



CC consisting essentially of at least one hepatitis C virus (HCV) NS3/4a  
 CC conformational epitope and a multiple epitope fusion antigen (MEPA),  
 CC bound to the support. The NS3/4a conformational epitope and/or MEPA  
 CC reacts specifically with anti-HCV antibodies present in a biological  
 CC sample from an HCV-infected individual. The immunoassay of the invention  
 CC is useful for detecting hepatitis C virus infection in a biological  
 CC sample. The method of the invention provides a sensitive, accurate  
 CC diagnostic and prognostic tool to provide adequate patient care and to  
 CC prevent transmission of HCV by blood and by blood products, or by  
 CC personal contact. Use of NS3/4a conformational epitope in combination  
 CC with MEPA, provides a sensitive and reliable method for detecting early  
 CC HCV seroconversion. Use of MEPA has the added advantages of decreasing  
 CC masking problems, improving sensitivity in detecting antibodies by  
 CC allowing a greater number of epitopes on a unit surface area of  
 CC substrate, and improving substrate. Detection accuracy is increased and  
 CC the incidence of false results is reduced because of the identification  
 CC and the use of highly immunogenic HCV antigens which are present during  
 CC the early stages of HCV seroconversion. The present amino acid sequence  
 CC represents the non-structural protein NS3/4a conformational epitope of  
 CC the invention  
 CC

XX Sequence 686 AA;

Query Match 100.0%; Score 3619; DB 5; Length 686;

Best Local Similarity 100.0%; Pred. No. 1.6e-306; Mismatches 0; Gaps 0;

Matches 686; Conservative 0; Indels 0;

1 MAPITAAOQTRGLGCIITSLTGRDNQVEGEVOIVSTAOTFLATCINGCVCTVYHGA 60  
 1 MAPITAAOQTRGLGCIITSLTGRDNQVEGEVOIVSTAOTFLATCINGCVCTVYHGA 60  
 61 GTRITASPCKGVIOYMTNVDLGVMPAPQSGSRSLTPTCGSSSDLYLTRADVIPIVRR 120  
 61 GTRITASPCKGVIOYMTNVDLGVMPAPQSGSRSLTPTCGSSSDLYLTRADVIPIVRR 120  
 61 GTRITASPCKGVIOYMTNVDLGVMPAPQSGSRSLTPTCGSSSDLYLTRADVIPIVRR 120  
 121 GDSRGSLSPPRISYLGSSGGLCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETMM 180  
 121 GDSRGSLSPPRISYLGSSGGLCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETMM 180  
 121 GDSRGSLSPPRISYLGSSGGLCPAGHAGVIFRAAVCTRGVAKAVDFIPVENLETMM 180  
 181 RSPVPTNDSPPVPOSFVHAPGSGSTVPAAYAOQKVLVLANSVAAITGFG 240  
 181 RSPVPTNDSPPVPOSFVHAPGSGSTVPAAYAOQKVLVLANSVAAITGFG 240  
 181 RSPVPTNDSPPVPOSFVHAPGSGSTVPAAYAOQKVLVLANSVAAITGFG 240  
 181 RSPVPTNDSPPVPOSFVHAPGSGSTVPAAYAOQKVLVLANSVAAITGFG 240  
 241 AYMKAHGIDPNIRGTGVTITGSPITSTYTGKFLADGCGGAVDIIIDCEHSTDATS 300  
 241 AYMKAHGIDPNIRGTGVTITGSPITSTYTGKFLADGCGGAVDIIIDCEHSTDATS 300  
 241 AYMKAHGIDPNIRGTGVTITGSPITSTYTGKFLADGCGGAVDIIIDCEHSTDATS 300  
 241 AYMKAHGIDPNIRGTGVTITGSPITSTYTGKFLADGCGGAVDIIIDCEHSTDATS 300  
 301 ILGIGTVLDQETAGARLVLAATPPGSVTPHPNIEVALSTTGEIPFGAKIPIEVI 360  
 301 ILGIGTVLDQETAGARLVLAATPPGSVTPHPNIEVALSTTGEIPFGAKIPIEVI 360  
 301 ILGIGTVLDQETAGARLVLAATPPGSVTPHPNIEVALSTTGEIPFGAKIPIEVI 360  
 301 ILGIGTVLDQETAGARLVLAATPPGSVTPHPNIEVALSTTGEIPFGAKIPIEVI 360  
 361 KGGHILFCHSKKKCDLAAKLVAGINAVYRGLDVSVPIPGDVVVAATDMLMGYT 420  
 361 KGGHILFCHSKKKCDLAAKLVAGINAVYRGLDVSVPIPGDVVVAATDMLMGYT 420  
 361 KGGHILFCHSKKKCDLAAKLVAGINAVYRGLDVSVPIPGDVVVAATDMLMGYT 420  
 361 KGGHILFCHSKKKCDLAAKLVAGINAVYRGLDVSVPIPGDVVVAATDMLMGYT 420  
 421 GDFPSVIDCMTCTQTVDFSLDPTFTIETITLPODAVSRTORGRGKGIYFPAVG 480  
 421 GDFPSVIDCMTCTQTVDFSLDPTFTIETITLPODAVSRTORGRGKGIYFPAVG 480  
 421 GDFPSVIDCMTCTQTVDFSLDPTFTIETITLPODAVSRTORGRGKGIYFPAVG 480  
 421 GDFPSVIDCMTCTQTVDFSLDPTFTIETITLPODAVSRTORGRGKGIYFPAVG 480  
 481 ERPSGMPFSSVLCCEYDAGCAWELTPAETTVRLAAMTQGLPYCOHLEFWEVFGGL 540  
 481 ERPSGMPFSSVLCCEYDAGCAWELTPAETTVRLAAMTQGLPYCOHLEFWEVFGGL 540  
 481 ERPSGMPFSSVLCCEYDAGCAWELTPAETTVRLAAMTQGLPYCOHLEFWEVFGGL 540  
 481 ERPSGMPFSSVLCCEYDAGCAWELTPAETTVRLAAMTQGLPYCOHLEFWEVFGGL 540  
 541 THIDHNFISORROGSENPYLVAQATVCAQAQAPPSMDQWKKLILKFTLHGPFTLL 600  
 541 THIDHNFISORROGSENPYLVAQATVCAQAQAPPSMDQWKKLILKFTLHGPFTLL 600  
 541 THIDHNFISORROGSENPYLVAQATVCAQAQAPPSMDQWKKLILKFTLHGPFTLL 600  
 541 THIDHNFISORROGSENPYLVAQATVCAQAQAPPSMDQWKKLILKFTLHGPFTLL 600  
 601 YRLGAVONEITLTHPTVKIMTQMSADLEVVTSTWLVGVVLAALAAVCLSTGCVVIYGR 660  
 601 YRLGAVONEITLTHPTVKIMTQMSADLEVVTSTWLVGVVLAALAAVCLSTGCVVIYGR 660  
 601 YRLGAVONEITLTHPTVKIMTQMSADLEVVTSTWLVGVVLAALAAVCLSTGCVVIYGR 660  
 601 YRLGAVONEITLTHPTVKIMTQMSADLEVVTSTWLVGVVLAALAAVCLSTGCVVIYGR 660  
 661 VTLGSKPAILIPREVLYRPFDEMERC 686  
 661 VTLGSKPAILIPREVLYRPFDEMERC 686

Db 661 VTLGSKPAILIPREVLYRPFDEMERC 686

# RESULT 2

AAE18689  
 AAE18689 standard; protein; 686 AA.

AC AAE18689;  
 XX

DT 17-MAY-2002 (first entry)

XX HCV-1 NS3/4a mutant conformational antigen.

XX Hepatitis C virus; NS3/4a antigen; HCV infection; mutant; mutein.

XX Hepatitis C virus type 1.

OS Synthetic.

XX Key Location/Qualifiers

FT MISC-difference 403 /note="Wild type Thr substituted with Pro"

FT MISC-difference 404 /note="Wild type Ser substituted with Ile"

XX WO200196875-A2.

XX 20-DEC-2001.

XX 14-JUN-2001; 2001WO-US019369.

XX 15-JUN-2000; 2000US-0212082P.

XX 02-APR-2001; 2001US-0280811P.

XX 02-APR-2001; 2001US-0280867P.

XX (CHIR) CHIRON CORP.

XX Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;

XX Medina-Selby A;

XX WPI: 2002-179522/23.

XX N-PSDB: AAD29795.

XX Immunassay solid support useful for detecting hepatitis C virus

XX infection in a biological sample, comprises at least one of HCV anti-core

XX antibody and HCV NS3/4a epitope, bound to the support.

XX Example 2; Fig 4; 87pp; English.

XX The present invention relates to hepatitis C virus (HCV) core antigen and

XX NS (nonstructural) 3/4a antibody combination assay that can detect both

XX HCV antigens and antibodies present in a sample using a single solid

XX matrix as well as immunoassay solid supports for use in the assay. The

XX solid support is useful for detecting HCV infection in a biological

XX sample. The present sequence is HCV-1 NS3/4a mutant conformational

XX antigen. This sequence is used in the exemplification of the invention

XX

XX

XX

XX

XX



CC matrix as well as immunoassay solid supports for use in the assay. The  
CC solid support is useful for detecting HCV infection in a biological  
CC sample. The present sequence is MEFA (multiple epitope fusion antigen) 12  
CC protein. This sequence is used in the exemplification of the invention  
XX  
XX Sequence 829 AA;

Query Match 100.0%; Score 4455; DB 5; Length 829;  
Best Local Similarity 100.0%; Pred. No. 1,7e-310;  
Matches 829; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATRAVCYLKDDGPGVQGIINFEOKESNGPVKWSIKGLTGLHGFHYHEFGDNTAGCTS 60  
DB 1 MATRAVCYLKDDGPGVQGIINFEOKESNGPVKWSIKGLTGLHGFHYHEFGDNTAGCTS 60  
QY 61 AGPHFNPLSTRGNCSTYPGHITGHRAMKLGSAARTTSGVSLFAPAKONETHVTGGA 120  
DB 61 AGPHFNPLSTRGNCSTYPGHITGHRAMKLGSAARTTSGVSLFAPAKONETHVTGGA 120  
QY 121 AARTTSGTSLFSPGASONTIOLITSTDNSSPPVVPQSFQVLAHLAFTSGSKTVPAAYA 180  
DB 121 AARTTSGTSLFSPGASONTIOLITSTDNSSPPVVPQSFQVLAHLAFTSGSKTVPAAYA 180  
QY 181 AOGKTVLVNPSVAATLGFAYMSKAGIDPNIRITGVTITTSPTITVYTGKFLADGCG 240  
DB 181 AOGKTVLVNPSVAATLGFAYMSKAGIDPNIRITGVTITTSPTITVYTGKFLADGCG 240  
QY 241 SGGAVIDIICDECHSTADTSLIGTGTVDQAEATGABVLAATPPGSAVPPHNEEV 300  
DB 241 SGGAVIDIICDECHSTADTSLIGTGTVDQAEATGABVLAATPPGSAVPPHNEEV 300  
QY 301 ALSTTGEIPFYGKAIPLFVIGKGRHLIFCHSKKCDLAAKLVAGINAVAYVGLDVS 360  
DB 301 ALSTTGEIPFYGKAIPLFVIGKGRHLIFCHSKKCDLAAKLVAGINAVAYVGLDVS 360  
QY 361 IPTSGDVVVAATDMLMTGYTDPDSVIDONTACSGKPAIIPDRVLYREFDEMEECSQH 420  
DB 361 IPTSGDVVVAATDMLMTGYTDPDSVIDONTACSGKPAIIPDRVLYREFDEMEECSQH 420  
QY 421 LPTIEQGMWLABOFKQKALGSRGSKPAIVPDKVLYOQYDEMEECSQAAPYIEQAOVIA 480  
DB 421 LPTIEQGMWLABOFKQKALGSRGSKPAIVPDKVLYOQYDEMEECSQAAPYIEQAOVIA 480  
QY 481 HQFEKVLGLIDNDQVVTDPKELIYEAPEDEMEECASRAALIEBQORMAEMLSKIQGL 540  
DB 481 HQFEKVLGLIDNDQVVTDPKELIYEAPEDEMEECASRAALIEBQORMAEMLSKIQGL 540  
QY 541 GILRRHVGPBGCAVOVMNRLLAFASRGHVSFTHYVSRSRFAOLPVMARPDYNNPLV 600  
DB 541 GILRRHVGPBGCAVOVMNRLLAFASRGHVSFTHYVSRSRFAOLPVMARPDYNNPLV 600  
QY 601 ETWKKPDEVPPVHGRSSRRFAOLPVMARPDYNNPLVETWKKPDEVPPVHGRKTKNT 660  
DB 601 ETWKKPDEVPPVHGRSSRRFAOLPVMARPDYNNPLVETWKKPDEVPPVHGRKTKNT 660  
QY 661 NRRPDVVPFGGQIVGVYLLPRRGPRLGLVATRTKTPIPKARRPEGRITWAOGPYMWL 720  
DB 661 NRRPDVVPFGGQIVGVYLLPRRGPRLGLVATRTKTPIPKARRPEGRITWAOGPYMWL 720  
QY 721 YGNKDRSTGSKWGPYPMRPKTKNTNRRPDYVFGGQIVGVYLLPRRGPRLGLV 780  
DB 721 YGNKDRSTGSKWGPYPMRPKTKNTNRRPDYVFGGQIVGVYLLPRRGPRLGLV 780  
QY 781 ATRKTSIPKARRPEGRITWAOGPYMWLYGNKDRSTGSKWGPYPM 829  
DB 781 ATRKTSIPKARRPEGRITWAOGPYMWLYGNKDRSTGSKWGPYPM 829

RESULT 2  
ID ADC06769 standard: protein; 829 AA.  
AC ADC06769;

XX 18-DEC-2003 (first entry)  
XX Chimeric multiple epitope fusion antigen 12 protein.  
DE  
XX  
XX immunoassay solid support; HCV; NS3/4a; non-structural;  
KW non-A, non-B hepatitis; NANB; multiple epitope fusion antigen 12; MEFA12;  
XX chimeric.  
XX  
XX Chimeric.  
OS Synthetic.  
OS Unidentified.  
OS Hepatitis C virus.  
OS Homo sapiens.  
XX US2002192639-A1.  
XX  
XX 19-DEC-2002.  
XX  
XX 14-JUN-2001; 2001US-00881239.  
XX  
XX 15-JUN-2000; 2000US-0212082P.  
XX 02-APR-2001; 2001US-0280811P.  
XX 02-APR-2001; 2001US-0280867P.  
XX  
XX (CHIE/) CHIEN D Y.  
XX (ARCA/) ARCANDEL L.  
XX (TAND/) TANDESKE L.  
XX (GEOR/) GEORGE-NASCIMENTO C.  
XX (COIT/) COIT D.  
XX (MED/) MEDINA-SELBY A.  
XX  
XX Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;  
XX Medina-Selby A;  
XX WPI; 2003-644609/61.  
XX N-PSDB; ADC06770.  
XX  
XX Immunoassay solid support for detecting hepatitis C virus infection in  
PT biological samples, comprises a hepatitis C virus anti-core antibody and  
PT an isolated hepatitis C virus NS3/4a epitope bound HCV anti-core  
XX antibody.  
XX  
XX Claim 45; Fig 7; 40pp; English.  
XX  
XX The invention relates to a novel immunoassay solid support comprising at  
CC least one hepatitis C virus (HCV) anti-core antibody and at least one  
CC isolated HCV NS3/4a (non-structural protein 3/4a) epitope bound thereo.  
CC The system of the invention may be useful for detecting HCV infection in  
CC a biological sample and for treating or detecting non-A, non-B hepatitis  
CC (NANB hepatitis). The current sequence is that of the chimeric multiple  
CC epitope fusion antigen 12 (MEFA12) protein of the invention.  
XX  
XX  
XX Sequence 829 AA;

Query Match 100.0%; Score 4455; DB 7; Length 829;  
Best Local Similarity 100.0%; Pred. No. 1,7e-310;  
Matches 829; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATRAVCYLKDDGPGVQGIINFEOKESNGPVKWSIKGLTGLHGFHYHEFGDNTAGCTS 60  
DB 1 MATRAVCYLKDDGPGVQGIINFEOKESNGPVKWSIKGLTGLHGFHYHEFGDNTAGCTS 60  
QY 61 AGPHFNPLSTRGNCSTYPGHITGHRAMKLGSAARTTSGVSLFAPAKONETHVTGGA 120  
DB 61 AGPHFNPLSTRGNCSTYPGHITGHRAMKLGSAARTTSGVSLFAPAKONETHVTGGA 120  
QY 121 AARTTSGTSLFSPGASONTIOLITSTDNSSPPVVPQSFQVLAHLAFTSGSKTVPAAYA 180  
DB 121 AARTTSGTSLFSPGASONTIOLITSTDNSSPPVVPQSFQVLAHLAFTSGSKTVPAAYA 180  
QY 181 AOGKTVLVNPSVAATLGFAYMSKAGIDPNIRITGVTITTSPTITVYTGKFLADGCG 240  
DB 181 AOGKTVLVNPSVAATLGFAYMSKAGIDPNIRITGVTITTSPTITVYTGKFLADGCG 240

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: June 21, 2004, 10:18:09 ; Search time 65.5868 Seconds  
(without alignments)  
4734.482 Million cell updates/sec

Title: US-10-658-782-6

Perfect score: 5912  
Sequence: 1 MATKAVCVLKGDPVQGIIN.....GNKDRSTGKSWKPGYFMP 1099

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneeqp1980s:\*  
2: geneeqp1990s:\*  
3: geneeqp2000s:\*  
4: geneeqp2001s:\*  
5: geneeqp2002s:\*  
6: geneeqp2003as:\*  
7: geneeqp2003bs:\*  
8: geneeqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5912	100.0	1099	5	AAU76378
2	5912	100.0	1099	6	ABG72262
3	4032	68.2	829	7	AAE18690
4	4032	68.2	829	7	ADCO6769
5	3829.5	64.8	1021	2	AAW34481
6	3829.5	64.8	1021	2	AAW40039
7	3829.5	64.8	1021	5	AAE22050
8	3050.5	51.6	841	2	AAE68547
9	3050.5	51.6	841	6	ABO27020
10	3050.5	51.6	841	7	ADA07875
11	3047.5	51.5	841	2	AAW01701
12	3047.5	51.5	841	2	AAW46397
13	3047.5	51.5	841	2	AAW97609
14	3042.5	49.2	2261	1	AAE14349
15	2909.5	49.2	2261	1	AAE90164
16	2909.5	49.2	2261	1	AAE92050
17	2909.5	49.2	2261	1	AAE90288
18	2909.5	49.2	2261	1	AAE90288
19	2909.5	49.2	2261	1	AAE90288
20	2909.5	49.2	2261	1	AAE90288
21	2909.5	49.2	2261	1	AAE90288
22	2909.5	49.2	2261	1	AAE90288
23	2909.5	49.2	2261	1	AAE90288
24	2909.5	49.2	2261	1	AAE90288
25	2906.5	49.2	2301	1	AAE92047

26	2906.5	49.2	2772	2	AAE08123	AAE08123 Hepatitis
27	2900.5	49.1	3011	5	AAE08123	AAE08123 Hepatitis
28	2900.5	49.1	3011	5	AAE08123	AAE08123 Hepatitis
29	2897.5	49.0	1766	2	AAE25135	AAE25135 HCV poly
30	2896.5	49.0	1766	2	AAE25135	AAE25135 HCV poly
31	2895.5	48.9	2894	2	AAE24440	AAE24440 Hepatitis
32	2893.5	48.9	2894	2	AAE24440	AAE24440 Hepatitis
33	2891.5	48.9	3011	2	AAE31621	AAE31621 HCV-1 pol
34	2890.5	48.9	1766	2	AAE90158	AAE90158 Protein s
35	2890.5	48.9	2894	2	AAE70230	AAE70230 Composite
36	2888.5	48.8	2436	2	AAE28582	AAE28582 Hepatitis
37	2880.5	48.7	2955	2	AAE08124	AAE08124 Hepatitis
38	2877.5	48.7	3011	5	AAE2052	AAE2052 Hepatitis
39	2875	48.6	3011	2	AAE77397	AAE77397 Hepatitis
40	2875	48.6	3011	6	ABP71460	ABP71460 Amino aci
41	2875	48.6	3012	5	AAU99289	AAU99289 Hepatitis
42	2875	48.6	3012	6	ABU61848	ABU61848 HCV H77 c
43	2868	48.5	2984	4	AAE00442	AAE00442 Hepatitis
44	2868	48.5	3011	2	AAE77398	AAE77398 Hepatitis
45	2868	48.5	3011	2	AAE98021	AAE98021 Infection

## ALIGNMENTS

## RESULT 1

AAU76378 standard; protein; 1099 AA.

AAU76378;

08-MAY-2002 (first entry)

HCV multiple epitope fusion antigen (MEFA) 7.1 protein sequence.

Hepatitis C virus; HCV; NS3/4a conformational epitope; seroconversion;

immunoassay solid support; multiple epitope fusion antigen; MEFA;

non-structural protein.

Hepatitis C virus.

Synthetic.

WO200196870-A2.

14-JUN-2001; 2001WO-05019156.

15-JUN-2000; 2000US-0212082P.

02-APR-2001; 2001US-0280811P.

02-APR-2001; 2001US-0280867P.

(CHIR) CHIRON CORP.

Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;

Medina-Selby A.

WPI, 2002-090228/12.

N-PSDB; ABR15345.

Immunosay solid support, useful for detecting hepatitis C virus

infection in biological sample, comprises HCV NS3/4a conformational

epitope and multiple epitope fusion antigen bound to the support.

Claim 5; Fig 5; 92pp; English.

The present invention relates to a new immunoassay solid support

consisting essentially of at least one hepatitis C virus (HCV) NS3/4a

conformational epitope and a multiple epitope fusion antigen (MEFA),  
bound to the support. The NS3/4a conformational epitope and/or MEFA  
reacts specifically with anti-HCV antibodies present in a biological  
sample from an HCV-infected individual. The immunoassay of the invention  
is useful for detecting hepatitis C virus infection in a biological

SEX ID NO: 6

Sequence 1099 AA;

<b>Qy</b>	1 MATAAVCVLTAGDGPVGIIINEEQKESNGPVAKWGISLGLTEGHHGFHVEFGNTACTGS 60
<b>Dz</b>	1 MATAAVCVLKGDGPVGIIINEEQKESNGPVAKWGISLGLTEGHGFFHVEFGNTACTGS 60

QY 6 L A G H F N P L S R K H G G P K D E E R H V G D L G N T A D K G V A D V S I E D S V I S L S G D H C I I G R T I V 120

Dd 61 A G H F N P L S R K H G G P K D E E R H V G D L G N T A D K G V A D V S I E D S V I S L S G D H C I I G R T I V 120

Db  
121 HEKADDLGKGNSESTKTGNAGSRLACGVIGIAQNLSGNCSTYPGHTTGRMAWKLG 180

181 AARTTSGFVSLFAPGAKONETHVCGAAARTTSGILSLFSGASQNIQLIVDFIVENTLE 240

241 TTKRSPPVPTDSSPPVVFQFVAHLHAPGSGSKTKVPAAYAAQGVKVLVLPNSVAATL 300

Dd

301 GGAATMCAAGCDDPDKRTGVRITTTGGSPITYSTYKFLADGGSCSGAYDIIICDECHSTD 360

Db 361 ATSTLGISTVLDDAETAGARLVLTATATPPGSVTVPHNIEEVALSTTGEIPFYKAIP L 420

Db

421 EVIKGGRIIFCHSKKKCEIAAKLVALGNAVAYYRGLDVSVIPISGDVVVAITDALMT 480

481 CVTQDENDEVTDCNTCTMOTMTECF DDDMMETMTAT DDSSVVGSDGAAAGAAA

Db 481 GYTGDFSDVIDNCNTCVTQWDFSLDPTFLETITLPQDAISRTQRRGRTGKPGIYRFV 540

Dd  
541 AGERPSCMFSSVLC EYDAGCAYELTPAETTYRLRAYNTTGLPVCCOHLFEFNEGV 600

601 TGLTHIDAHFLSQTQSGENLPYIVAYQATVCARAQAPPSWDQWKKCLIRLKPTLHGPT 660

661 PLYLRGAVQNEITLTHTETKTIINTCMSADLEVVTSA<sup>CS</sup>CKPAITPDREVLYREFDEMEE 720  
721 CSQHPPIYECGMMLAEQFKOKALGLSRGCKPAITPDKEVLYOYDEMEEC<sup>SOA</sup>APYTFCA 780

721 CSOHPYIEQNMWLAEPFKXALGLSRGKPAIVPDKEVLYQQIDEMECCQAAPYIEQA 780

RESULT 2  
ABG72262  
ID ABG72262 standard; protein; 1099 AA  
XX

AC	ABG72262;
XX	
DT	06-MAR-2003 (first entry)
XX	

DE	Immunoblot support; Hepatitis C Virus type-1
KV	NS3/4a conformational epitome: multiple amino acids
KW	NS3/4a conformational epitome: multiple amino acids
XX	Immunoblot support; Hepatitis C Virus type-1
YY	NS3/4a conformational epitome: multiple amino acids
ZZ	NS3/4a conformational epitome: multiple amino acids

XX mutant; mutein.

05	Hepatitis C virus type 1
05	Hepatitis C virus type 2
05	Hepatitis C virus type 3
05	Synthetic.

	Key Region
XX	
FH	
FT	

Region	FT	FT	FT
--------	----	----	----

FT	FT	FT	FT	Region
FT	FT	FT	FT	

Region	FT	FT	FT	FT
--------	----	----	----	----

Region	FT	FT	FT
Region	FT	FT	FT

Region	FT	FT	FT
--------	----	----	----

FT	Region
FT	
FT	

location/Offsets

1. 156

/note= "Correspond to amino acids 1-156 of HCV-1 NSD superoxide dismutase"

159. 116

/note= "Correspond to amino acids 303-320 of HCV-1 E1"

179. 189

/note= "Correspond to consensus sequence of amino acids 390-410 of HCV-1 E2 HVR"

200. 230

/note= "Correspond to consensus sequence of amino acids 384-414 of HCV-1 and HCV-2 E2 HVR"

231. 696

/note= "Correspond to amino acids 1193-1658 of HCV-1 helicase"

699. 745

/note= "Correspond to amino acids 1689-1735 of HCV-1 E1 epitope"

748. 794

/note= "Correspond to amino acids 1689-1735 of HCV-3 5-1-1 epitope"

797. 843

/note= "Correspond to amino acids 1689-1735 of HCV-2 5-1-1 epitope"

846. 881

/note= "Correspond to amino acids 1901-1936 of HCV-1